

## SEQUENCE LISTING

<110> Paul O. Sheppard  
Si Lok

<120> Mammalian Secretory Protein Zsig43

<130> 98-15C1

<150> 60/109,915

<151> 1998-11-23

<150> 09/440,484

<151> 1999-11-15

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<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 3015

<212> DNA

<213> Homo sapiens

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<221> CDS

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Arg Leu Leu Pro Leu Leu Gly Leu Leu Leu Gly Ser Ala Ser Arg Ala	
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ccc ggc aag tcg ccg ccg gag ccc ccc agc ccg cag gag atc ctg atc	146
Pro Gly Lys Ser Pro Pro Glu Pro Pro Ser Pro Gln Glu Ile Leu Ile	
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aag gtg cag gtg tat gtg agc ggg gag ctg gtg ccc ctg gcc cgg gcc	194

tca	gtg	gat	gtg	ttt	ggg	aac	cgg	act	ctg	ctg	gca	gct	ggc	acc	aca	242
Ser	Val	Asp	Val	Phe	Gly	Asn	Arg	Thr	Leu	Leu	Ala	Ala	Gly	Thr	Thr	
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Asp	Ser	Glu	Gly	Val	Ala	Thr	Leu	Pro	Leu	Ser	Tyr	Arg	Leu	Gly	Thr	
				80					85					90		
tgg	gtg	ctg	gtc	act	gct	gcc	cgc	cct	ggc	ttc	ctc	acc	aac	tct	gtg	338
Trp	Val	Leu	Val	Thr	Ala	Ala	Arg	Pro	Gly	Phe	Leu	Thr	Asn	Ser	Val	
			95					100					105			
ccc	tgg	cgt	gtt	gac	aag	ctg	ccc	ttg	tat	gcg	tct	gtc	agc	ctc	tac	386
Pro	Trp	Arg	Val	Asp	Lys	Leu	Pro	Leu	Tyr	Ala	Ser	Val	Ser	Leu	Tyr	
		110					115					120				
ctg	ctc	cct	gag	cgg	ccg	gcc	acg	ctc	atc	ctc	tat	gag	gac	ctg	gtg	434
Leu	Leu	Pro	Glu	Arg	Pro	Ala	Thr	Leu	Ile	Leu	Tyr	Glu	Asp	Leu	Val	
		125				130					135					
cac	att	ctc	cta	ggc	tct	ccc	ggt	gcc	cgc	tcc	cag	ccc	ttg	gtg	cag	482
His	Ile	Leu	Leu	Gly	Ser	Pro	Gly	Ala	Arg	Ser	Gln	Pro	Leu	Val	Gln	
140					145					150					155	
ttc	cag	cgc	cgg	gct	gcc	cgc	ctg	cct	gtc	agc	tcc	acc	tac	agc	cag	530
Phe	Gln	Arg	Arg	Ala	Ala	Arg	Leu	Pro	Val	Ser	Ser	Thr	Tyr	Ser	Gln	
				160					165					170		
ctc	tgg	gcg	tca	ctt	acg	cct	gcc	agc	acc	cag	cag	gaa	atg	cgg	gct	578
Leu	Trp	Ala	Ser	Leu	Thr	Pro	Ala	Ser	Thr	Gln	Gln	Glu	Met	Arg	Ala	
			175					180					185			
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Phe	Pro	Ala	Phe	Leu	Gly	Thr	Glu	Ala	Ser	Ser	Ser	Gly	Asn	Gly	Ser	
		190					195					200				
tgg	ctg	gag	ctg	atg	ccc	ctg	act	gct	gtg	agc	gtg	cac	ctg	ctg	aca	674
Trp	Leu	Glu	Leu	Met	Pro	Leu	Thr	Ala	Val	Ser	Val	His	Leu	Leu	Thr	
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Gly Asn Gly Thr Glu Val Pro Leu Ser Gly Pro Ile His Leu Ser Leu	
220 225 230 235	
ccc gtg ccc tcc gag act cgt gcc ctc acc gtg ggc acc agc att cca	770
Pro Val Pro Ser Glu Thr Arg Ala Leu Thr Val Gly Thr Ser Ile Pro	
240 245 250	
gcc tgg aga ttt gac ccc aag agt ggg ctg tgg gtg cgc aat ggc act	818
Ala Trp Arg Phe Asp Pro Lys Ser Gly Leu Trp Val Arg Asn Gly Thr	
255 260 265	
ggg gta atc cgg aag gaa ggc cgg cag ctc tac tgg acc ttc gtc tcc	866
Gly Val Ile Arg Lys Glu Gly Arg Gln Leu Tyr Trp Thr Phe Val Ser	
270 275 280	
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Pro Gln Leu Gly Tyr Trp Val Ala Ala Met Ala Ser Pro Thr Ala Gly	
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ctg gtc acc atc acg tcg ggc atc cag gac atc ggc acc tac cac acc	962
Leu Val Thr Ile Thr Ser Gly Ile Gln Asp Ile Gly Thr Tyr His Thr	
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atc ttc ttg ctc acc atc ctg gca gcc ctg gcc ctg ctg gtg ctt atc	1010
Ile Phe Leu Leu Thr Ile Leu Ala Ala Leu Ala Leu Leu Val Leu Ile	
320 325 330	
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Leu Leu Cys Leu Leu Ile Tyr Tyr Cys Arg Arg Arg Cys Leu Lys Pro	
335 340 345	
agg caa cag cac cgc aag ctg cag ctc tcg ggg ccc tct gac ggt aac	1106
Arg Gln Gln His Arg Lys Leu Gln Leu Ser Gly Pro Ser Asp Gly Asn	
350 355 360	
aaa cga gac cag gcc acc tcg atg tcc cag ctc cac ctc atc tgt ggg	1154
Lys Arg Asp Gln Ala Thr Ser Met Ser Gln Leu His Leu Ile Cys Gly	
365 370 375	
gga ccc ctg gaa ccc gcc ccg tcg ggg gac ccc gag gct ccg cct cca	1202
Gly Pro Leu Glu Pro Ala Pro Ser Gly Asp Pro Glu Ala Pro Pro Pro	
380 385 390 395	

1250

1298

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1394

1442

1490

1538

1586

1634

1682

1730

Ala Gly Val Gly Asp Glu Pro Ala Pro Pro Glu Gly Thr Ala Pro Gly	
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Pro Ala Arg Ala Phe Pro Gln Pro Asp Pro Gln Arg Pro Gln Met Pro	
575 580 585	
ggc cac tcg ggc ccg ggg ggc gag ggc ggc ggg ggc ggc ggc gag ggc	1826
Gly His Ser Gly Pro Gly Gly Glu Gly Gly Gly Gly Gly Gly Glu Gly	
590 595 600	
tgg ggg gcc ggg cgc gcg gcg ccc gtc agt ggc tca gtc acc atc cct	1874
Trp Gly Ala Gly Arg Ala Ala Pro Val Ser Gly Ser Val Thr Ile Pro	
605 610 615	
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Val Leu Phe Asn Glu Ser Thr Met Ala Gln Leu Asn Gly Glu Leu Gln	
620 625 630 635	
gcc ctg acc gag aag aag ctg ctg gaa ctg ggc gtg aag ccg cac ccg	1970
Ala Leu Thr Glu Lys Lys Leu Leu Glu Leu Gly Val Lys Pro His Pro	
640 645 650	
cgc gcc tgg ttc gtg tcc ctc gac ggg cgc tcc aac tcg caa gtg cgc	2018
Arg Ala Trp Phe Val Ser Leu Asp Gly Arg Ser Asn Ser Gln Val Arg	
655 660 665	
cac tct tac atc gac ctg cag gcg ggc ggc ggg gca cgc agc acc gac	2066
His Ser Tyr Ile Asp Leu Gln Ala Gly Gly Gly Ala Arg Ser Thr Asp	
670 675 680	
gcc agc ctg gac tcg ggc gta gat gtc cac gag gcg ccg ccc gcg cgc	2114
Ala Ser Leu Asp Ser Gly Val Asp Val His Glu Ala Arg Pro Ala Arg	
685 690 695	
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Arg Arg Pro Ala Arg Glu Glu Arg Glu Arg Ala Pro Pro Ala Ala Pro	
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ccg ccg ccg ccc gcg ccc ccg cgc ctg gcg ctc agc gag gac acg gag	2210
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65				70					75					80	
Ala	Thr	Leu	Pro	Leu	Ser	Tyr	Arg	Leu	Gly	Thr	Trp	Val	Leu	Val	Thr
				85				90						95	
Ala	Ala	Arg	Pro	Gly	Phe	Leu	Thr	Asn	Ser	Val	Pro	Trp	Arg	Val	Asp
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Lys	Leu	Pro	Leu	Tyr	Ala	Ser	Val	Ser	Leu	Tyr	Leu	Leu	Pro	Glu	Arg
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145				150						155					160
Ala	Arg	Leu	Pro	Val	Ser	Ser	Thr	Tyr	Ser	Gln	Leu	Trp	Ala	Ser	Leu
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Thr	Pro	Ala	Ser	Thr	Gln	Gln	Glu	Met	Arg	Ala	Phe	Pro	Ala	Phe	Leu
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Gly	Thr	Glu	Ala	Ser	Ser	Ser	Gly	Asn	Gly	Ser	Trp	Leu	Glu	Leu	Met
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225				230						235					240
Thr	Arg	Ala	Leu	Thr	Val	Gly	Thr	Ser	Ile	Pro	Ala	Trp	Arg	Phe	Asp
				245					250					255	
Pro	Lys	Ser	Gly	Leu	Trp	Val	Arg	Asn	Gly	Thr	Gly	Val	Ile	Arg	Lys
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Trp	Val	Ala	Ala	Met	Ala	Ser	Pro	Thr	Ala	Gly	Leu	Val	Thr	Ile	Thr
	290					295					300				
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305				310						315					320
Ile	Leu	Ala	Ala	Leu	Ala	Leu	Leu	Val	Leu	Ile	Leu	Leu	Cys	Leu	Leu
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Ile	Tyr	Tyr	Cys	Arg	Arg	Arg	Cys	Leu	Lys	Pro	Arg	Gln	Gln	His	Arg
			340					345					350		

Lys Leu Gln Leu Ser Gly Pro Ser Asp Gly Asn Lys Arg Asp Gln Ala  
 355 360 365  
 Thr Ser Met Ser Gln Leu His Leu Ile Cys Gly Gly Pro Leu Glu Pro  
 370 375 380  
 Ala Pro Ser Gly Asp Pro Glu Ala Pro Pro Pro Gly Pro Leu His Ser  
 385 390 395 400  
 Ala Phe Ser Ser Ser Arg Asp Leu Ala Ser Ser Arg Asp Asp Phe Phe  
 405 410 415  
 Arg Thr Lys Pro Arg Ser Ala Ser Arg Pro Ala Ala Glu Pro Ser Gly  
 420 425 430  
 Ala Arg Gly Gly Glu Ser Ala Gly Leu Lys Gly Ala Arg Ser Ala Glu  
 435 440 445  
 Gly Pro Gly Gly Leu Glu Pro Gly Leu Glu Glu His Arg Arg Gly Pro  
 450 455 460  
 Ser Gly Ala Ala Ala Phe Leu His Glu Pro Pro Ser Pro Pro Pro Pro  
 465 470 475 480  
 Phe Asp His Tyr Leu Gly His Lys Gly Ala Ala Glu Gly Lys Thr Pro  
 485 490 495  
 Asp Phe Leu Leu Ser Gln Ser Val Asp Gln Leu Ala Arg Pro Pro Ser  
 500 505 510  
 Leu Gly Gln Ala Gly Gln Leu Ile Phe Cys Gly Ser Ile Asp His Leu  
 515 520 525  
 Lys Asp Asn Val Tyr Arg Asn Val Met Pro Thr Leu Val Ile Pro Ala  
 530 535 540  
 His Tyr Val Arg Leu Gly Gly Glu Ala Gly Ala Ala Gly Val Gly Asp  
 545 550 555 560  
 Glu Pro Ala Pro Pro Glu Gly Thr Ala Pro Gly Pro Ala Arg Ala Phe  
 565 570 575  
 Pro Gln Pro Asp Pro Gln Arg Pro Gln Met Pro Gly His Ser Gly Pro  
 580 585 590  
 Gly Gly Glu Gly Gly Gly Gly Gly Glu Gly Trp Gly Ala Gly Arg  
 595 600 605  
 Ala Ala Pro Val Ser Gly Ser Val Thr Ile Pro Val Leu Phe Asn Glu  
 610 615 620  
 Ser Thr Met Ala Gln Leu Asn Gly Glu Leu Gln Ala Leu Thr Glu Lys  
 625 630 635 640  
 Lys Leu Leu Glu Leu Gly Val Lys Pro His Pro Arg Ala Trp Phe Val  
 645 650 655  
 Ser Leu Asp Gly Arg Ser Asn Ser Gln Val Arg His Ser Tyr Ile Asp  
 660 665 670  
 Leu Gln Ala Gly Gly Gly Ala Arg Ser Thr Asp Ala Ser Leu Asp Ser  
 675 680 685

1003388-102401



Gly Val Asp Val His Glu Ala Arg Pro Ala Arg Arg Arg Pro Ala Arg  
 690 695 700  
 Glu Glu Arg Glu Arg Ala Pro Pro Ala Ala Pro Pro Pro Pro Pro Ala  
 705 710 715 720  
 Pro Pro Arg Leu Ala Leu Ser Glu Asp Thr Glu Pro Ser Ser Ser Glu  
 725 730 735  
 Ser Arg Thr Gly Leu Cys Ser Pro Glu Asp Asn Ser Leu Thr Pro Leu  
 740 745 750  
 Leu Asp Glu Val Ala Ala Pro Glu Gly Arg Ala Ala Thr Val Pro Arg  
 755 760 765  
 Gly Arg Gly Arg Ser Arg Gly Asp Ser Ser Arg Ser Ser Ala Ser Glu  
 770 775 780  
 Leu Arg Arg Asp Ser Leu Thr Ser Pro Glu Asp Glu Leu Gly Ala Glu  
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<210> 3  
 <211> 2478  
 <212> DNA  
 <213> Artificial Sequence

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<221> variation  
 <222> (1)...(2478)  
 <223> N is any nucleotide.

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athytnatha	argtncargt	ntaygtwnsn	ggngarytng	tnccnytnge	nmngncnwsn	180
gtngaygtnt	tyggnaaymg	nacnytnytn	gcngcnggna	cnacngayws	ngarggngtn	240
gcnacnytn	cnytnwsnta	ymgnytnngn	acntgggtny	tngtnacngc	ngcnmgncn	300
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athytnytn	gnwsnccngg	ngcnmgwnsn	carccnytn	tncarttyca	rmgngmngcn	480
gcnmgnytn	cngtnwsnws	nacntaywsn	carytnctgg	cnwsnytnac	nccngcnwsn	540
acncarcarg	aratgmngc	nttyccngcn	ttytnggna	cngargcnws	nwsnwsnggn	600

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&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer

&lt;400&gt; 4

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48

<210> 5  
 <211> 291  
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<220>  
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<221> variation  
 <222> (1)...(1)  
 <223> N is any nucleotide.

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ccccccancc	cgcacgagat	cctgatcaag	gtgcaggtgt	atgtgagcgg	ggagctggtg	180
cccctggccc	gggcctcact	ggatgtgttt	gggaaccgga	ctctgctggc	agctggcacc	240
acanactcat	agggtgtggc	ccnccctgcc	cctcagttat	cgcttgggca	c	291